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SEQUENCE LISTING

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<120> A METHOD FOR IMPROVING THE THERMOSTABILITY OF SUCROSE PHOSPHORYLASE (SP)

<130> EG014US

<140> PCT/JP2004/012533

<141> 2004-08-31

<150> JP2003-313305

<151> 2003-09-04

<160> 27

<170> PatentIn version 3.3

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gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta	336
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Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
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Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
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145 150 155 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
165 170 175

Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
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Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
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Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
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245 250 255

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Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
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Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
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Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
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Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 375 380

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Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
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Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
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Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly	
20 25 30	
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Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met	
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Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys	
85 90 95	
gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gct ctc ttt tta	336
Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu	
100 105 110	
aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta	384
Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val	
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gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtg	432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val	
130 135 140	
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	180	185	190	
gat gcc ttt gct tat	gca gtg aag aaa ttg	gat act aat gat ttc ttt		624
Asp Ala Phe Ala Tyr	Ala Val Lys Leu	Asp Thr Asn Asp Phe	Phe	
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Gly Thr Thr Glu Ile	Glu Thr Pro Thr	Ala His Ser Ile Val	Ile Lys	
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Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
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Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu
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Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
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Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
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Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
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Asp Phe Gln Glu Lys Lys Asp Ala Ser Asp Tyr Ala Asp Leu Phe Leu
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Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Lys
 165 170 175

Lys Asn Ile Glu His Leu Ala Val Asn Gly Cys Asp Leu Ile Arg Leu
 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
 195 200 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Thr Lys Val Gln Thr Ile Ala
 210 215 220

Lys Glu Ala Gly Ala Asp Ile Leu Pro Glu Ile His Glu His Tyr Ser
 225 230 235 240

Ile Gln Phe Lys Ile Ala Glu His Asp Tyr Phe Ile Tyr Asp Phe Ala
 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Arg Val Gln Arg
 260 265 270

Leu Ala Asp Trp Leu Ala Lys Ser Pro Met Lys Gln Phe Thr Thr Leu
 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
290 295 300

Asp Glu Glu Ile Ala Tyr Thr Ser Asp Gln Leu Tyr Lys Val Gly Ala
305 310 315 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
325 330 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
340 345 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
355 360 365

Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
370 375 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

Ser Glu Glu Ile Ala His Glu Val Glu Arg Pro Val Val Lys Ala Leu
405 410 415

Ile Lys Leu Phe Ser Tyr Arg Asn Asn Ser Gln Ala Phe Asp Leu Asp
420 425 430

Gly Ser Leu Glu Thr Glu Val Leu Asp Asp His Thr Ile Val Ile Lys
435 440 445

Arg Ser Asn Gln Asp Lys Ser Ala Leu Ala Gln Ala Val Ile Asn Leu
450 455 460

Gln Asp Leu Thr Tyr Gln Val Thr Glu Asn Gly Gln Thr Ile Thr Phe
465 470 475 480

Glu

<210> 7
<211> 1470
<212> DNA
<213> Leuconostoc mesenteroides

<220>
<221> CDS
<222> (1)..(1470)

<400> 7	
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Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu	
1 5 10 15	
ggc aaa aac tta aaa gat gtt cat caa gtc ttg aaa gaa gat att gga	96
Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly	
20 25 30	
gat gcg att ggt ggg gtt cat ttg ttg cct ttc ttc cct tca aca ggt	144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly	
35 40 45	
gat gcg ggt ttt gcg cca gcc gat tat act cgt gtt gat gcc gca ttt	192
Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe	
50 55 60	
ggt gat tgg gca gat gtc gaa gca ttg ggt gaa gaa tac tat ttg atg	240
Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met	
65 70 75 80	
ttt gac ttc atg att aac cat att tct cgt gaa tca gtg atg tat caa	288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln	

85	90	95	
gat ttt aag aag aat cat gac gat tca aag tat aaa gat ttc ttt att Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile 100 105 110			336
cgt tgg gaa aag ttc tgg gca aag gcc ggc gaa aac cgt cca aca caa Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln 115 120 125			384
gcc gat gtt gac tta att tac aag cgt aaa gat aag gca cca acg caa Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln 130 135 140			432
gaa atc act ttt gat gat ggc aca aca gaa aac ttg tgg aat act ttt Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe 145 150 155 160			480
ggg gaa gaa caa att gac att gat gtt aat tca gcc att gcc aag gaa Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu 165 170 175			528
ttt att aag aca acc ctt gaa gac atg gta aaa cat ggt gct aac ttg Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu 180 185 190			576
att cgt ttg gat gcc ttt gcg tat gca gtt aaa aaa gtt gac aca aat Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn 195 200 205			624
gac ttc ttc gtt gag cca gaa atc tgg gac act ttg aat gaa gta cgt Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg 210 215 220			672
gaa att ttg aca cca tta aag gct gaa att tta cca gaa att cat gaa Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu 225 230 235 240			720
cat tac tca atc cct aaa aag atc aat gat cat ggt tac ttc acc tat His Tyr Ser Ile Thr Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr 245 250 255			768
gac ttt gca tta cca atg aca acg ctt tac aca ttg tat tca ggt aag Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys 260 265 270			816
aca aat caa ttg gca aag tgg ttg aag atg tca cca atg aag caa ttc Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe 275 280 285			864
aca aca ttg gac acg cat gat ggt att ggt gtc gtt gat gcc cgt gat Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp 290 295 300			912
att cta act gat gat gaa att gac tac gct tct gaa caa ctt tac aag Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys 305 310 315 320			960
gtt ggc gcg aat gtc aaa aag aca tat tca tct gct tca tac aac aac Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn 325 330 335			1008
ctt gat att tac caa att aac tca act tat tat tca gca ttg gga aat Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn 340 345 350			1056
gat gat gca gca tac ttg ttg agt cgt gtc ttc caa gtc ttt gcg cct Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro 355 360 365			1104
gga att cca caa att tat tac gtt ggt ttg ttg gca ggt gaa aac gat Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp 370 375 380			1152
atc gcg ctt ttg gag tca act aaa gaa ggt cgt aat att aac cgt cat Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His 385 390 395 400			1200
tac tat acg cgt gaa gaa gtt aag tca gaa gtt aag cga cca gtt gtt Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val 405 410 415			1248
gct aac tta ttg aag cta ttg tca tgg cgt aat gaa agc cct gca ttt Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe 420 425 430			1296

gat ttg gct ggc tca atc aca gtt gac acg cca act gat aca aca att 1344
 Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
 435 440 445

gtg gtg aca cgt caa gat gaa aat ggt caa aac aaa gct gta tta aca 1392
 Val Val Thr Arg Gln Asp Glu Asn Gly Gln Asn Lys Ala Val Leu Thr
 450 455 460

gcc gat gcg gcc aac aaa act ttt gaa atc gtt gag aat ggt caa act 1440
 Ala Asp Ala Ala Asn Lys Thr Phe Glu Ile Val Glu Asn Gly Gln Thr
 465 470 475 480

gtt atg agc agt gat aat ttg act cag aac 1470
 Val Met Ser Ser Asp Asn Leu Thr Gln Asn
 485 490

<210> 8
 <211> 490
 <212> PRT
 <213> Leuconostoc mesenteroides

<400> 8

Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
 1 5 10 15

Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp Ile Gly
 20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
 35 40 45

Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe
 50 55 60

Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met
 65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln
 85 90 95

Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile
 100 105 110

Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln
 115 120 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln
 130 135 140

Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe
 145 150 155 160

Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu
 165 170 175

Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu
 180 185 190

Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn
 195 200 205

Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg
 210 215 220

Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu
 225 230 235 240

His Tyr Ser Ile Pro Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr
245 250 255

Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys
260 265 270

Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe
275 280 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
290 295 300

Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys
305 310 315 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn
325 330 335

Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
340 345 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
355 360 365

Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
370 375 380

Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His
385 390 395 400

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val
405 410 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe
420 425 430

Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
435 440 445

Val Val Thr Arg Gln Asp Glu Asn Gly Gln Asn Lys Ala Val Leu Thr
450 455 460

Ala Asp Ala Ala Asn Lys Thr Phe Glu Ile Val Glu Asn Gly Gln Thr
465 470 475 480

Val Met Ser Ser Asp Asn Leu Thr Gln Asn
485 490

<210> 9
<211> 1467
<212> DNA
<213> Oenococcus oeni

<220>
<221> CDS
<222> (1)..(1467)

<400> 9
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Met Pro Val Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Met
1 5 10 15
ggt aag aat atc aag gaa tta caa tac att tta gat aaa tat att gga 96
Gly Lys Asn Ile Lys Glu Leu Gln Tyr Ile Leu Asp Lys Tyr Ile Gly
20 25 30
gac gcg att ggt gga gtt cat ctg ctg cct ttt ttt ccg tca acc gga 144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly

35	40	45	
gat cgt ggt ttt gcg ccc tgc gat tac act cgt gtc aat ccg gat ttc Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asn Pro Asp Phe 50 55 60			192
ggt gat tgg gag gat gtc gag gaa ctt gga aaa aag tat tat tta atg Gly Asp Trp Glu Asp Val Glu Glu Leu Gly Lys Lys Tyr Tyr Leu Met 65 70 75 80			240
ttt gat ttc atg att aat cac att tcc cgt gaa tgc att atg tat caa Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Ile Met Tyr Gln 85 90 95			288
gat ttc aag gaa aaa aag gat gct tcc agc tac aag gac ttt ttt att Asp Phe Lys Glu Lys Lys Asp Ala Ser Ser Tyr Lys Asp Phe Phe Ile 100 105 110			336
cgt tgg gaa aag ttc tgg ccg aaa gga cgc ccg acg aag gcc gat atc Arg Trp Glu Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Ala Asp Ile 115 120 125			384
gat tta att tac aaa aga aaa gat aag cgc ccg att cag ggg att act Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln Gly Ile Thr 130 135 140			432
ttt gca gac ggc agt caa gaa cat ctt tgg aat act ttt ggc gat gag Phe Ala Asp Gly Ser Gln Glu His Leu Trp Asn Thr Phe Gly Asp Glu 145 150 155 160			480
cag atc gat att aac gtg aag tcc aaa gtt gct cag gaa ttt ttt aaa Gln Ile Asp Ile Asn Val Lys Ser Lys Val Ala Gln Glu Phe Phe Lys 165 170 175			528
gat act tta cag tca atg gtt aag cac ggt gcg gat ttg att cgc ctg Asp Thr Leu Gln Ser Met Val Lys His Gly Ala Asp Leu Ile Arg Leu 180 185 190			576
gat gcc ttt gct tat gca att aaa aag att gat act aat gac ttc ttt Asp Ala Phe Ala Tyr Ala Ile Lys Lys Ile Asp Thr Asn Asp Phe Phe 195 200 205			624
att gaa ccg gaa att tgg gat tta ctg gaa tca gtt cgg aag att ctc Ile Glu Pro Glu Ile Trp Asp Leu Leu Glu Ser Val Arg Lys Ile Leu 210 215 220			672
gac ccc cta cat gct gaa att tta ccg gaa att tat gaa cat tac aca Asp Pro Leu His Ala Glu Ile Leu Pro Glu Ile Tyr Glu His Tyr Thr 225 230 235 240			720
atc ccg gcc aaa ata aat gag tat ggt tac ttt acc tat gat ttt gtt Ile Pro Ala Lys Ile Asn Glu Tyr Gly Tyr Phe Thr Tyr Asp Phe Val 245 250 255			768
tta cct ctg gta att ttg tac act ctt tat tct gga aat ccc aag caa Leu Pro Leu Val Ile Leu Tyr Thr Leu Tyr Ser Gly Asn Pro Lys Gln 260 265 270			816
ttg gcc aaa tgg ttg aaa atg tca cca aaa aaa cag ttt acg act ctt Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gln Phe Thr Thr Leu 275 280 285			864
gat act cat gat gga atc ggg gtt gtt gat gct cgc gat att tta act Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Thr 290 295 300			912
gat gag gaa atc gac tat act tcc agt gaa ctg tat aaa gtt ggt gcg Asp Glu Glu Ile Asp Tyr Thr Ser Ser Glu Leu Tyr Lys Val Gly Ala 305 310 315 320			960
aac gtc aaa ccg act tat tca tct gcg gcc tat aat aat ttg gat att Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp Ile 325 330 335			1008
tac cag att aac tgc acc tat tat tca gct ctt ggc aat gat gac aaa Tyr Gln Ile Asn Ser Thr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350			1056
gcc tat ttg ctt gcc cgt gca ata caa att ttt gcc ccg gga att cca Ala Tyr Leu Leu Ala Arg Ala Ile Gln Ile Phe Ala Pro Gly Ile Pro 355 360 365			1104
caa atc tat tac gca ggc ctg ctg gct ggt gaa aac gat ttg gat ttg Gln Ile Tyr Tyr Ala Gly Leu Leu Ala Gly Glu Asn Asp Leu Asp Leu 370 375 380			1152

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ttg gaa aag acc aag gaa gga cgc aat ata aat cgt cat tat tac agt 1200
Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

gaa gaa gaa gtt gcc aat gaa gtg cag aga cca att gtt gcc tgc cta 1248
Glu Glu Glu Val Ala Asn Glu Val Gln Arg Pro Ile Val Ala Cys Leu
405 410 415

ctg aaa ttg ttg gct tgg cgc aat cgc agt gcc gct ttt gat ctt caa 1296
Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gln
420 425 430

gga gat att caa gtc agc gca acc gac aaa aat gaa atc aaa att att 1344
Gly Asp Ile Gln Val Ser Ala Thr Asp Lys Asn Glu Ile Lys Ile Ile
435 440 445

cga act tca acc aat ggc caa gac acc gcg gaa tta acc gct aat gtg 1392
Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val
450 455 460

gct cta aaa acc ttt act ata aag gaa aat gat aaa att att tta att 1440
Ala Leu Lys Thr Phe Thr Ile Lys Glu Asn Asp Lys Ile Ile Leu Ile
465 470 475 480

gaa gat cag act gat aca aag gat atc 1467
Glu Asp Gln Thr Asp Thr Lys Asp Ile
485

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<210> 10
 <211> 489
 <212> PRT
 <213> Oenococcus oeni

<400> 10

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Met Pro Val Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Met
1 5 10 15

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Gly Lys Asn Ile Lys Glu Leu Gln Tyr Ile Leu Asp Lys Tyr Ile Gly
20 25 30

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Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

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Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asn Pro Asp Phe
50 55 60

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Gly Asp Trp Glu Asp Val Glu Glu Leu Gly Lys Lys Tyr Tyr Leu Met
65 70 75 80

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Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Ile Met Tyr Gln
85 90 95

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Asp Phe Lys Glu Lys Lys Asp Ala Ser Ser Tyr Lys Asp Phe Phe Ile
100 105 110

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Arg Trp Glu Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Ala Asp Ile
115 120 125

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Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln Gly Ile Thr
130 135 140

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Phe Ala Asp Gly Ser Gln Glu His Leu Trp Asn Thr Phe Gly Asp Glu
145 150 155 160

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Gln Ile Asp Ile Asn Val Lys Ser Lys Val Ala Gln Glu Phe Phe Lys
165 170 175

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Asp Thr Leu Gln Ser Met Val Lys His Gly Ala Asp Leu Ile Arg Leu
180 185 190

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Asp Ala Phe Ala Tyr Ala Ile Lys Lys Ile Asp Thr Asn Asp Phe Phe
 195 200 205

Ile Glu Pro Glu Ile Trp Asp Leu Leu Glu Ser Val Arg Lys Ile Leu
 210 215 220

Asp Pro Leu His Ala Glu Ile Leu Pro Glu Ile Tyr Glu His Tyr Thr
 225 230 235 240

Ile Pro Ala Lys Ile Asn Glu Tyr Gly Tyr Phe Thr Tyr Asp Phe Val
 245 250 255

Leu Pro Leu Val Ile Leu Tyr Thr Leu Tyr Ser Gly Asn Pro Lys Gln
 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gln Phe Thr Thr Leu
 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Thr
 290 295 300

Asp Glu Glu Ile Asp Tyr Thr Ser Ser Glu Leu Tyr Lys Val Gly Ala
 305 310 315 320

Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp Ile
 325 330 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
 340 345 350

Ala Tyr Leu Leu Ala Arg Ala Ile Gln Ile Phe Ala Pro Gly Ile Pro
 355 360 365

Gln Ile Tyr Tyr Ala Gly Leu Leu Ala Gly Glu Asn Asp Leu Asp Leu
 370 375 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
 385 390 395 400

Glu Glu Glu Val Ala Asn Glu Val Gln Arg Pro Ile Val Ala Cys Leu
 405 410 415

Leu Lys Leu Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gln
 420 425 430

Gly Asp Ile Gln Val Ser Ala Thr Asp Lys Asn Glu Ile Lys Ile Ile
 435 440 445

Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val
 450 455 460

Ala Leu Lys Thr Phe Thr Ile Lys Glu Asn Asp Lys Ile Ile Leu Ile
 465 470 475 480

Glu Asp Gln Thr Asp Thr Lys Asp Ile
 485

<210> 11
 <211> 1446
 <212> DNA
 <213> Streptococcus mitis

<220>
 <221> CDS
 <222> (1)..(1446)


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<400> 11
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Met Pro Ile Gln Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu
1      5      10      15

gga aat aat ctt aaa gac tta tat gag aat ttg gaa gag tat ttt gga      96
Gly Asn Asn Leu Lys Asp Leu Tyr Glu Asn Leu Glu Glu Tyr Phe Gly
20      25      30

gat gct att ggg gga gtt cac ctt cta cca ttt ttc cca tca aca ggt      144
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35      40      45

gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gat tca gct ttt      192
Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
50      55      60

ggt gat tgg gag gat gtt aag cgt tta ggt gag aaa tat tat ctt atg      240
Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65      70      75

ttt gac ttt atg att aat cat att tct cgt caa tct aag tat tat aag      288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
85      90      95

gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gat ctc ttt tta      336
Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Asp Leu Phe Leu
100     105     110

aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta      384
Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
115     120     125

gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtt      432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
130     135     140

ttt gaa gat ggg tca gtc gaa cat ttg tgg aat acc ttt ggt gag gag      480
Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145     150     155

cag att gat ctt gat gtg acc aaa gaa gta act atg gaa ttt atc cgt      528
Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
165     170     175

aag acc att cag cac ttg gca agt aat ggg tgt gat ttg att cgt cta      576
Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
180     185     190

gac gcc ttt gct tat gca gtg aag aaa ttg gat act aat gat ttc ttt      624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
195     200     205

gta gaa cca gat att tgg gat tta ttg gac aaa gtt cga gat atc gct      672
Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
210     215     220

gct gag tat ggg aca gag ctc tta cct gag att cat gaa cat tat tcg      720
Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225     230     235

att cag ttt aaa ata gca gac cat gat tac tat gtt tat gat ttt gct      768
Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
245     250     255

ctt cca atg gtg aca ctt tat act ctt tac agt tcc aga aca gag cgt      816
Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
260     265     270

ttg gct aag tgg tta aag atg agc cca atg aag caa ttt acg acg cta      864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
275     280     285

gac acc cat gat ggg att gga gtg gtg gat gtc aag gat atc ttg aca      912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
290     295     300

gat gag gag att gac tat gct tca aat gaa ctc tat aag gtt gga gct      960
Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305     310     315

aat gtc aaa cgt aag tac tcc agt gcc gag tat aat aat tta gat atc      1008
Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
325     330     335

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tac caa atc aat tca acc tat tat tct gcg ctt gga gat gat gat gtc 1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
340 345 350

aag tat ttc ctt gca cga tta att caa gca ttt gct cca ggt att cct 1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
355 360 365

caa gtt tac tat gta ggt cta tta gca ggc aag aat gat ttg aaa tta 1152
Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
370 375 380

tta gaa gaa act aaa gta ggt cga aat att aat cgt cat tac tat agc 1200
Leu Glu Glu Thr Lys Val Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

aat gag gaa ata gca gaa gaa gtc caa cgt cct gta gtg aag gcc ctt 1248
Asn Glu Glu Ile Ala Glu Glu Val Gln Arg Pro Val Val Lys Ala Leu
405 410 415

ctc aat cta ttt tct ttc cgt aat cga tca gta gca ttt gat tta gaa 1296
Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu
420 425 430

gga act att gac gtt gaa aca cca aca gcc cac agc att gta atc aaa 1344
Gly Thr Ile Asp Val Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
435 440 445

cgt caa aat aaa gat aag tcc gta aca gca gta gca gaa att gat ttg 1392
Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Ala Glu Ile Asp Leu
450 455 460

caa aat cag act tat cga gta atg aga acg gaa tgg aag tac att ttg 1440
Gln Asn Gln Thr Tyr Arg Val Met Arg Thr Glu Trp Lys Tyr Ile Leu
465 470 475 480

aag act 1446
Lys Thr

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<210> 12
<211> 482
<212> PRT
<213> Streptococcus mitis

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<400> 12

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Met Pro Ile Gln Asn Lys Thr Met Leu Ile Thr Tyr Ser Asp Ser Leu
1 5 10 15

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Gly Asn Asn Leu Lys Asp Leu Tyr Glu Asn Leu Glu Glu Tyr Phe Gly
20 25 30

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Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

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Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe
50 55 60

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Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65 70 75 80

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Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
85 90 95

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Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Asp Leu Phe Leu
100 105 110

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Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val
115 120 125

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Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Val
130 135 140

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Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145 150 155 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe Ile Arg
165 170 175

Lys Thr Ile Gln His Leu Ala Ser Asn Gly Cys Asp Leu Ile Arg Leu
180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205

Val Glu Pro Asp Ile Trp Asp Leu Leu Asp Lys Val Arg Asp Ile Ala
210 215 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225 230 235 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
245 250 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg
260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
290 295 300

Asp Glu Glu Ile Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala
305 310 315 320

Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile
325 330 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Val
340 345 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
355 360 365

Gln Val Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu
370 375 380

Leu Glu Glu Thr Lys Val Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

Asn Glu Glu Ile Ala Glu Glu Val Gln Arg Pro Val Val Lys Ala Leu
405 410 415

Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu
420 425 430

Gly Thr Ile Asp Val Glu Thr Pro Thr Ala His Ser Ile Val Ile Lys
435 440 445

Arg Gln Asn Lys Asp Lys Ser Val Thr Ala Val Ala Glu Ile Asp Leu
450 455 460

Gln Asn Gln Thr Tyr Arg Val Met Arg Thr Glu Trp Lys Tyr Ile Leu
465 470 475 480

Lys Thr

<210> 13
 <211> 1458
 <212> DNA
 <213> Leuconostoc mesenteroides

<220>
 <221> CDS
 <222> (1)..(1458)

<400> 13
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 Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
 1 5 10 15
 ggc agt aat atc aag gaa gtc cac caa gtt ttg aag gaa gac att ggc 96
 Gly Ser Asn Ile Lys Glu Val His Gln Val Leu Lys Glu Asp Ile Gly
 20 25 30
 gat gcg att ggc ggg gta cat ttg tta cca ttt ttc cct tct aca ggt 144
 Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
 35 40 45
 gat cgt ggc ttc gcc cct tct gat tac acg cgt gtt gat gca aca ttt 192
 Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asp Ala Thr Phe
 50 55 60
 ggt gat tgg aat gat gtt gag gca ctt ggg caa gaa tac tat ttg atg 240
 Gly Asp Trp Asn Asp Val Glu Ala Leu Gly Gln Glu Tyr Tyr Leu Met
 65 70 75 80
 ttt gat ttt atg atc aat cat att tct cgt gaa tcg gag atg tat caa 288
 Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Glu Met Tyr Gln
 85 90 95
 gat ttt aaa gca aat cac gat caa tca aag tac cgt gat ttc ttc att 336
 Asp Phe Lys Ala Asn His Asp Gln Ser Lys Tyr Arg Asp Phe Phe Ile
 100 105 110
 cgc tgg gaa aag ttt tgg caa cag gct ggg cca gat cga cca act caa 384
 Arg Trp Glu Lys Phe Trp Gln Gln Ala Gly Pro Asp Arg Pro Thr Gln
 115 120 125
 gca gac gtc gac ctt att tat aag cgc aaa gac aag gcg cca att caa 432
 Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln
 130 135 140
 gaa atc act ttt gct gac ggt acg aca gag cat ctt tgg aat aca ttt 480
 Glu Ile Thr Phe Ala Asp Gly Thr Thr Glu His Leu Trp Asn Thr Phe
 145 150 155 160
 ggt gaa gaa caa att gat att gat gtt aat tct caa att gct aaa gcc 528
 Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Gln Ile Ala Lys Ala
 165 170 175
 ttc att aaa gca acg cta gaa gac atg gtc caa cat ggt gcc aat ttg 576
 Phe Ile Lys Ala Thr Leu Glu Asp Met Val Gln His Gly Ala Asn Leu
 180 185 190
 att cgt tta gat gct ttc gcc tat gct gtt aag aaa gtt ggg aca aat 624
 Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn
 195 200 205
 gat ttc ttt gtc gaa cca gaa ata tgg act gtt tta aac gaa gtg cgt 672
 Asp Phe Phe Val Glu Pro Glu Ile Trp Thr Val Leu Asn Glu Val Arg
 210 215 220
 gac att ttg gca cct atg cat gct gaa att tta cca gaa att cat gag 720
 Asp Ile Leu Ala Pro Met His Ala Glu Ile Leu Pro Glu Ile His Glu
 225 230 235 240
 cat tat aca att cct caa aag atc aac gcc cat ggt tat ttc act tat 768
 His Tyr Thr Ile Pro Gln Lys Ile Asn Ala His Gly Tyr Phe Thr Tyr
 245 250 255
 gat ttt gct ttg cca atg aca gta ctt tat acg ctt tac tca ggc aaa 816
 Asp Phe Ala Leu Pro Met Thr Val Leu Tyr Thr Leu Tyr Ser Gly Lys
 260 265 270
 aca aat cga cta gcc aac tgg ctc aaa cag tct ccg atg aaa caa ttc 864
 Thr Asn Arg Leu Ala Asn Trp Leu Lys Gln Ser Pro Met Lys Gln Phe
 275 280 285

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acg acg tta gat acg cat gat ggc att ggg gtt gtt gac gca cgt gat    912
Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
290 295 300

att ttg aca gac gaa gaa att gat tat gct tct gag gaa tta tac aaa    960
Ile Leu Thr Asp Glu Glu Ile Asp Tyr Ala Ser Glu Glu Leu Tyr Lys
305 310 315 320

gtt gga gcc aat gtc aaa aag acc tac tca tca gct gcg tat aat aac    1008
Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn
325 330 335

tta gat att tat cag att aat tca act tac tat tca gct tta ggc aat    1056
Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
340 345 350

gat gat gcc gca tat ttg ttg agt cgt gtt ttc caa gtc ttt gca cct    1104
Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
355 360 365

ggg att cca caa att tat tat gtc ggg tta ctt gca ggt gag aat gat    1152
Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
370 375 380

att gat ttg ttg gaa tct tca aaa gaa ggt cgt aat att aat cgt cat    1200
Ile Asp Leu Leu Glu Ser Ser Lys Glu Gly Arg Asn Ile Asn Arg His
385 390 395 400

tac tat act cgt gaa gaa ata aaa tca gct gtt aag cgg cca gtt gtt    1248
Tyr Tyr Thr Arg Glu Glu Ile Lys Ser Ala Val Lys Arg Pro Val Val
405 410 415

gct gac tta ttg gca tta tta tca tgg cgt aat cag ttt tca gca ttt    1296
Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gln Phe Ser Ala Phe
420 425 430

gct ctg gat ggg aca atc act gtc gag aca cca tca gaa cat gat att    1344
Ala Leu Asp Gly Thr Ile Thr Val Glu Thr Pro Ser Glu His Asp Ile
435 440 445

aaa att aca cga acg gat cat tcc gga gat aat ata gct att ttg cta    1392
Lys Ile Thr Arg Thr Asp His Ser Gly Asp Asn Ile Ala Ile Leu Leu
450 455 460

gct aat gcc aag aca cgc acc ttt gtc atc aca gca aat ggc aag aca    1440
Ala Asn Ala Lys Thr Arg Thr Phe Val Ile Thr Ala Asn Gly Lys Thr
465 470 475 480

gtc tta caa aac aaa taa
Val Leu Gln Asn Lys
485

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<210> 14
 <211> 485
 <212> PRT
 <213> Leuconostoc mesenteroides

<400> 14

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Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1 5 10 15

Gly Ser Asn Ile Lys Glu Val His Gln Val Leu Lys Glu Asp Ile Gly
20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Arg Val Asp Ala Thr Phe
50 55 60

Gly Asp Trp Asn Asp Val Glu Ala Leu Gly Gln Glu Tyr Tyr Leu Met
65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Glu Met Tyr Gln
85 90 95

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Asp Phe Lys Ala Asn His Asp Gln Ser Lys Tyr Arg Asp Phe Phe Ile
100 105 110

Arg Trp Glu Lys Phe Trp Gln Gln Ala Gly Pro Asp Arg Pro Thr Gln
115 120 125

Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Ile Gln
130 135 140

Glu Ile Thr Phe Ala Asp Gly Thr Thr Glu His Leu Trp Asn Thr Phe
145 150 155 160

Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Gln Ile Ala Lys Ala
165 170 175

Phe Ile Lys Ala Thr Leu Glu Asp Met Val Gln His Gly Ala Asn Leu
180 185 190

Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn
195 200 205

Asp Phe Phe Val Glu Pro Glu Ile Trp Thr Val Leu Asn Glu Val Arg
210 215 220

Asp Ile Leu Ala Pro Met His Ala Glu Ile Leu Pro Glu Ile His Glu
225 230 235 240

His Tyr Thr Ile Pro Gln Lys Ile Asn Ala His Gly Tyr Phe Thr Tyr
245 250 255

Asp Phe Ala Leu Pro Met Thr Val Leu Tyr Thr Leu Tyr Ser Gly Lys
260 265 270

Thr Asn Arg Leu Ala Asn Trp Leu Lys Gln Ser Pro Met Lys Gln Phe
275 280 285

Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
290 295 300

Ile Leu Thr Asp Glu Glu Ile Asp Tyr Ala Ser Glu Glu Leu Tyr Lys
305 310 315 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn
325 330 335

Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
340 345 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
355 360 365

Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
370 375 380

Ile Asp Leu Leu Glu Ser Ser Lys Glu Gly Arg Asn Ile Asn Arg His
385 390 395 400

Tyr Tyr Thr Arg Glu Glu Ile Lys Ser Ala Val Lys Arg Pro Val Val
405 410 415

Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gln Phe Ser Ala Phe
420 425 430

Ala Leu Asp Gly Thr Ile Thr Val Glu Thr Pro Ser Glu His Asp Ile

435

440

445

Lys Ile Thr Arg Thr Asp His Ser Gly Asp Asn Ile Ala Ile Leu Leu
450 455 460

Ala Asn Ala Lys Thr Arg Thr Phe Val Ile Thr Ala Asn Gly Lys Thr
465 470 475 480

Val Leu Gln Asn Lys
485

<210> 15
<211> 1443
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> CDS
<222> (1)..(1443)

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Met Lys Leu Gln Asn Lys Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu
1 5 10 15
ggt cat aat ttg aag gac ttg gat cat gta atg gat cgc tat ttt aat 96
Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn
20 25 30
aaa acg ata ggt ggt att cat tta tta cca ttt ttc cct tca aac ggt 144
Lys Thr Ile Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Asn Gly
35 40 45
gat cgc ggt ttt tct cct aca aga tat gat gta gtt gag cct aag ttt 192
Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
50 55 60
ggt tca tgg gaa gat gta gaa aag tta agt caa aag tat tat ttg atg 240
Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
65 70 75 80
ttt gac ttt atg att aat cat ctt tct aaa aaa tcc tca tat ttt gaa 288
Phe Asp Phe Met Ile Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu
85 90 95
gat ttt gaa gcc aag cac gat aaa agc aaa tat agc gat ctt ttc tta 336
Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu
100 105 110
agt tgg gat aaa ttt tgg cca aag ggc aga cca act aaa gaa gat ata 384
Ser Trp Asp Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile
115 120 125
gat tta att tat aaa cga aaa gat aag gcc cca tat caa aat att aaa 432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys
130 135 140
ttt gaa gat ggt act cat gaa aag atg tgg aat act ttc ggc cca gat 480
Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp
145 150 155 160
caa atg gat ttg gat gtt aga acc aag aca aca caa gat ttt ata aag 528
Gln Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys
165 170 175
cat aat tta caa aat ctt tct aaa cat ggt gct agt ttg att cgt tta 576
His Asn Leu Gln Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu
180 185 190
gat gca ttt gct tat gca att aaa aag tta gat aca aat gac ttc ttt 624
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205
gta gaa ccg gaa att tgg aat tta ctc gaa aag gta aat gat tat ctt 672
Val Glu Pro Glu Ile Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu
210 215 220
aaa gat act cca act act att ctg cct gaa att cat gag cat tat acg 720
Lys Asp Thr Pro Thr Thr Ile Leu Pro Glu Ile His Glu His Tyr Thr
225 230 235 240

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atg cca ttt aag gtg gca gaa cat gga tac ttt att tat gat ttt gct 768
Met Pro Phe Lys Val Ala Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala
245 250 255

tta cca atg gta ttg ttg tat tca ctt tat agc ggt aat agt act caa 816
Leu Pro Met Val Leu Leu Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln
260 265 270

ctt gct gct tgg cta aag aaa tgt ccg atg aag caa ttt act act tta 864
Leu Ala Ala Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
275 280 285

gat acc cac gat gga tta ggc gta gtt gac gca/aag gat att ctt acg 912
Asp Thr His Asp Gly Leu Gly Val Val Asp Ala Lys Asp Ile Leu Thr
290 295 300

gac gat caa att agc tac aca aca aac gaa ctt tat aaa att ggt gct 960
Asp Asp Gln Ile Ser Tyr Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala
305 310 315

aac gtc aag aag aaa tat tct agt gct gaa tat cat aat ttg gat att 1008
Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
325 330 335

tat caa att aat act act tat tat tct gca ttg ggt aat gat gat aaa 1056
Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
340 345 350

aaa tat ttt att gca cgg tta tta caa atc ttt gcc cct ggt att cca 1104
Lys Tyr Phe Ile Ala Arg Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro
355 360 365

caa att tat tat gtt gga ttg tta gca gga gaa aat gat att caa tta 1152
Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu
370 375 380

tta gag aag aca aaa gaa gga cgc gat att aat cgc cac tat tat gat 1200
Leu Glu Lys Thr Lys Glu Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp
385 390 395

ttg gat gag att gcg gaa caa gtt caa aga cct gta gta aaa tct ttg 1248
Leu Asp Glu Ile Ala Glu Gln Val Gln Arg Pro Val Val Lys Ser Leu
405 410 415

att aag tta ttg gaa ttt cgt aat tct gta cct gca ttt gat ttg gaa 1296
Ile Lys Leu Leu Glu Phe Arg Asn Ser Val Pro Ala Phe Asp Leu Glu
420 425 430

ggt tca atc aaa gtt gaa act cca agt gaa cat gaa att att gtc act 1344
Gly Ser Ile Lys Val Glu Thr Pro Ser Glu His Glu Ile Ile Val Thr
435 440 445

aga tca aat aag gca gga aca gaa gta gct agt acg tac gta gac ttt 1392
Arg Ser Asn Lys Ala Gly Thr Glu Val Ala Ser Thr Tyr Val Asp Phe
450 455 460

aag aac tta gac tat caa gtt aaa tac aat gat cag gtc ttt aat ttt 1440
Lys Asn Leu Asp Tyr Gln Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
465 470 475

tag 1443

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<210> 16
<211> 480
<212> PRT
<213> Lactobacillus acidophilus

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<400> 16

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Met Lys Leu Gln Asn Lys Ala Ile Leu Ile Thr Tyr Pro Asp Ser Leu
1 5 10 15

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Gly His Asn Leu Lys Asp Leu Asp His Val Met Asp Arg Tyr Phe Asn
20 25 30

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Lys Thr Ile Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Asn Gly
35 40 45

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Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
50 55 60

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Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
 65 70 75 80
 Phe Asp Phe Met Ile Asn His Leu Ser Lys Lys Ser Ser Tyr Phe Glu
 85 90 95
 Asp Phe Glu Ala Lys His Asp Lys Ser Lys Tyr Ser Asp Leu Phe Leu
 100 105 110
 Ser Trp Asp Lys Phe Trp Pro Lys Gly Arg Pro Thr Lys Glu Asp Ile
 115 120 125
 Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Tyr Gln Asn Ile Lys
 130 135 140
 Phe Glu Asp Gly Thr His Glu Lys Met Trp Asn Thr Phe Gly Pro Asp
 145 150 155 160
 Gln Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gln Asp Phe Ile Lys
 165 170 175
 His Asn Leu Gln Asn Leu Ser Lys His Gly Ala Ser Leu Ile Arg Leu
 180 185 190
 Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
 195 200 205
 Val Glu Pro Glu Ile Trp Asn Leu Leu Glu Lys Val Asn Asp Tyr Leu
 210 215 220
 Lys Asp Thr Pro Thr Thr Ile Leu Pro Glu Ile His Glu His Tyr Thr
 225 230 235 240
 Met Pro Phe Lys Val Ala Glu His Gly Tyr Phe Ile Tyr Asp Phe Ala
 245 250 255
 Leu Pro Met Val Leu Leu Tyr Ser Leu Tyr Ser Gly Asn Ser Thr Gln
 260 265 270
 Leu Ala Ala Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
 275 280 285
 Asp Thr His Asp Gly Leu Gly Val Val Asp Ala Lys Asp Ile Leu Thr
 290 295 300
 Asp Asp Gln Ile Ser Tyr Thr Thr Asn Glu Leu Tyr Lys Ile Gly Ala
 305 310 315 320
 Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
 325 330 335
 Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
 340 345 350
 Lys Tyr Phe Ile Ala Arg Leu Leu Gln Ile Phe Ala Pro Gly Ile Pro
 355 360 365
 Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp Ile Gln Leu
 370 375 380
 Leu Glu Lys Thr Lys Glu Gly Arg Asp Ile Asn Arg His Tyr Tyr Asp
 385 390 395 400

Leu Asp Glu Ile Ala Glu Gln Val Gln Arg Pro Val Val Lys Ser Leu
405 410 415

Ile Lys Leu Leu Glu Phe Arg Asn Ser Val Pro Ala Phe Asp Leu Glu
420 425 430

Gly Ser Ile Lys Val Glu Thr Pro Ser Glu His Glu Ile Ile Val Thr
435 440 445

Arg Ser Asn Lys Ala Gly Thr Glu Val Ala Ser Thr Tyr Val Asp Phe
450 455 460

Lys Asn Leu Asp Tyr Gln Val Lys Tyr Asn Asp Gln Val Phe Asn Phe
465 470 475 480

<210> 17
<211> 1443
<212> DNA
<213> Lactobacillus acidophilus

<220>
<221> CDS
<222> (1)..(1443)

<400> 17
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Met Pro Ile Glu Asn Lys Val Met Leu Ile Thr Tyr Pro Asp Ser Leu
1 5 10 15
ggt aaa aat tta aaa gaa tta gat gaa att tta agt gaa gac ttg aag 96
Gly Lys Asn Leu Lys Glu Leu Asp Glu Ile Leu Ser Glu Asp Leu Lys
20 25 30
ggg gct gta ggc ggt att cac tta ttg cca ttc ttc cca tca act ggt 144
Gly Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45
gac cgt gga ttt gct ccg act gga tat aca gaa gta gat cct aag ttt 192
Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe
50 55 60
ggt gat tgg tca gac att gaa aaa ata ggt aag aaa tat tat ttg atg 240
Gly Asp Trp Ser Asp Ile Glu Lys Ile Gly Lys Tyr Tyr Leu Met
65 70 75 80
ttt gat ttt atg att aat cat att tct cgt caa tca aaa ttt tat aaa 288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Phe Tyr Lys
85 90 95
gat ttc aaa caa aag aaa gat aaa agt aag tat gcc gat tta ttt ttg 336
Asp Phe Lys Gln Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu
100 105 110
agc tgg gac aaa ttt tgg ccg gaa ggt cgt cca act cga aaa gat att 384
Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile
115 120 125
gat tta att tat aaa cga aaa gat cgt gct cca tat caa gaa att act 432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gln Glu Ile Thr
130 135 140
ttt aca gat ggc agt aaa gaa aaa tta tgg aat act ttt ggt gaa gag 480
Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu
145 150 155 160
caa atc gat atg gat gtt cga aag gag gtg aca cag aag ttt att aaa 528
Gln Ile Asp Met Asp Val Arg Lys Glu Val Thr Gln Lys Phe Ile Lys
165 170 175
gat acg ttg aga gca tta att gat cat ggt gct gat att att cgg tta 576
Asp Thr Leu Arg Ala Leu Ile Asp His Gly Ala Asp Ile Ile Arg Leu
180 185 190
gat gct ttt gcg tat gct gta aag aag tta gat act aat gat ttc ttt 624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205
gta gag cca gaa att tgg gat tta cta aaa caa gta caa gat gat att 672

Val	Glu	Pro	Glu	Ile	Trp	Asp	Leu	Leu	Lys	Gln	Val	Gln	Asp	Asp	Ile		
210						215					220						
tct	gat	aaa	ggt	gca	atg	att	cta	cca	gaa	ata	cat	gaa	cac	tat	tca		720
Ser	Asp	Lys	Gly	Ala	Met	Ile	Leu	Pro	Glu	Ile	His	Glu	His	Tyr	Ser		
225					230					235					240		
atg	cca	ttt	aag	att	tca	aag	cat	gga	tat	tat	atc	tat	gac	ttt	gct		768
Met	Pro	Phe	Lys	Ile	Ser	Lys	His	Gly	Tyr	Tyr	Ile	Tyr	Asp	Phe	Ala		
				245					250					255			
tta	cca	atg	gta	act	tta	tat	tca	ctt	tat	tca	ggt	aag	tcc	aat	cgc		816
Leu	Pro	Met	Val	Thr	Leu	Tyr	Ser	Leu	Tyr	Ser	Gly	Lys	Ser	Asn	Arg		
			260					265					270				
tta	gct	gat	tgg	ctt	aag	aaa	tgt	cca	atg	aaa	cag	ttc	act	acc	tta		864
Leu	Ala	Asp	Trp	Leu	Lys	Lys	Cys	Pro	Met	Lys	Gln	Phe	Thr	Thr	Leu		
		275					280					285					
gat	aca	cat	gat	ggt	atc	ggt	gtt	gtt	gat	gct	cgt	gat	att	ctc	tcc		912
Asp	Thr	His	Asp	Gly	Ile	Gly	Val	Val	Asp	Ala	Arg	Asp	Ile	Leu	Ser		
290					295					300							
cct	gac	gaa	att	aaa	tac	aca	agt	aat	gaa	tig	tat	aaa	gtt	gga	gct		960
Pro	Asp	Glu	Ile	Lys	Tyr	Thr	Ser	Asn	Glu	Leu	Tyr	Lys	Val	Gly	Ala		
305				310						315				320			
aat	gtt	aaa	aag	aaa	tat	tct	agt	gcc	gaa	tat	cat	aat	tta	gat	atc		1008
Asn	Val	Lys	Lys	Lys	Tyr	Ser	Ser	Ala	Glu	Tyr	His	Asn	Leu	Asp	Ile		
				325					330					335			
tac	caa	att	aat	aca	act	tat	tat	tct	gct	tta	ggc	aat	gat	gat	aaa		1056
Tyr	Gln	Ile	Asn	Thr	Thr	Tyr	Tyr	Ser	Ala	Leu	Gly	Asn	Asp	Asp	Lys		
			340					345					350				
aaa	tac	ttt	att	gcg	aga	ctt	att	caa	atg	ttt	gcg	cct	ggt	att	ccg		1104
Lys	Tyr	Phe	Ile	Ala	Arg	Leu	Ile	Gln	Met	Phe	Ala	Pro	Gly	Ile	Pro		
		355				360					365						
caa	gtc	tat	tat	gta	gga	atg	ctg	gct	ggt	aaa	aac	gat	atc	gaa	ctc		1152
Gln	Val	Tyr	Tyr	Val	Gly	Met	Leu	Ala	Gly	Lys	Asn	Asp	Ile	Glu	Leu		
	370				375					380							
ctc	gaa	aag	act	aaa	gaa	ggt	aga	aac	att	aat	cgt	cat	tac	tat	ggc		1200
Leu	Glu	Lys	Thr	Lys	Glu	Gly	Arg	Asn	Ile	Asn	Arg	His	Tyr	Tyr	Gly		
385					390					395					400		
aga	gaa	gaa	gta	gct	gaa	gaa	act	aaa	aga	cct	tta	gta	gca	gca	ctc		1248
Arg	Glu	Glu	Val	Ala	Glu	Glu	Thr	Lys	Arg	Pro	Leu	Val	Ala	Ala	Leu		
			405						410				415				
tig	aaa	tig	ttt	aat	ttt	aga	aac	aat	gaa	gca	gct	ttt	gat	ctt	gat		1296
Leu	Lys	Leu	Phe	Asn	Phe	Arg	Asn	Asn	Glu	Ala	Ala	Phe	Asp	Leu	Asp		
		420						425					430				
gga	tcc	att	gaa	atc	act	acg	cct	aat	gaa	aac	gtg	att	caa	ata	act		1344
Gly	Ser	Ile	Glu	Ile	Thr	Thr	Pro	Asn	Glu	Asn	Val	Ile	Gln	Ile	Thr		
		435					440					445					
cgt	atg	aat	aaa	gat	aaa	act	cga	aaa	gca	aga	gct	gtt	att	aat	tta		1392
Arg	Met	Asn	Lys	Asp	Lys	Thr	Arg	Lys	Ala	Arg	Ala	Val	Ile	Asn	Leu		
	450					455					460						
aaa	aat	tta	act	tat	caa	gtg	act	gta	aat	aat	gag	gtt	att	aac	ttt		1440
Lys	Asn	Leu	Thr	Tyr	Gln	Val	Thr	Val	Asn	Asn	Glu	Val	Ile	Asn	Phe		
465					470					475					480		
taa																	1443

<210> 18
 <211> 480
 <212> PRT
 <213> Lactobacillus acidophilus

<400> 18

Met	Pro	Ile	Glu	Asn	Lys	Val	Met	Leu	Ile	Thr	Tyr	Pro	Asp	Ser	Leu
1				5				10						15	

Gly	Lys	Asn	Leu	Lys	Glu	Leu	Asp	Glu	Ile	Leu	Ser	Glu	Asp	Leu	Lys
		20					25						30		

Gly Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
 35 40 45
 Asp Arg Gly Phe Ala Pro Thr Gly Tyr Thr Glu Val Asp Pro Lys Phe
 50 55 60
 Gly Asp Trp Ser Asp Ile Glu Lys Ile Gly Lys Lys Tyr Tyr Leu Met
 65 70 75 80
 Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Phe Tyr Lys
 85 90 95
 Asp Phe Lys Gln Lys Lys Asp Lys Ser Lys Tyr Ala Asp Leu Phe Leu
 100 105 110
 Ser Trp Asp Lys Phe Trp Pro Glu Gly Arg Pro Thr Arg Lys Asp Ile
 115 120 125
 Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Tyr Gln Glu Ile Thr
 130 135 140
 Phe Thr Asp Gly Ser Lys Glu Lys Leu Trp Asn Thr Phe Gly Glu Glu
 145 150 155 160
 Gln Ile Asp Met Asp Val Arg Lys Glu Val Thr Gln Lys Phe Ile Lys
 165 170 175
 Asp Thr Leu Arg Ala Leu Ile Asp His Gly Ala Asp Ile Ile Arg Leu
 180 185 190
 Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
 195 200 205
 Val Glu Pro Glu Ile Trp Asp Leu Leu Lys Gln Val Gln Asp Asp Ile
 210 215 220
 Ser Asp Lys Gly Ala Met Ile Leu Pro Glu Ile His Glu His Tyr Ser
 225 230 235 240
 Met Pro Phe Lys Ile Ser Lys His Gly Tyr Tyr Ile Tyr Asp Phe Ala
 245 250 255
 Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Ser Asn Arg
 260 265 270
 Leu Ala Asp Trp Leu Lys Lys Cys Pro Met Lys Gln Phe Thr Thr Leu
 275 280 285
 Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Ile Leu Ser
 290 295 300
 Pro Asp Glu Ile Lys Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
 305 310 315 320
 Asn Val Lys Lys Lys Tyr Ser Ser Ala Glu Tyr His Asn Leu Asp Ile
 325 330 335
 Tyr Gln Ile Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys
 340 345 350
 Lys Tyr Phe Ile Ala Arg Leu Ile Gln Met Phe Ala Pro Gly Ile Pro
 355 360 365
 Gln Val Tyr Tyr Val Gly Met Leu Ala Gly Lys Asn Asp Ile Glu Leu

370 375 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Gly
385 390 395 400

Arg Glu Glu Val Ala Glu Glu Thr Lys Arg Pro Leu Val Ala Ala Leu
405 410 415

Leu Lys Leu Phe Asn Phe Arg Asn Asn Glu Ala Ala Phe Asp Leu Asp
420 425 430

Gly Ser Ile Glu Ile Thr Thr Pro Asn Glu Asn Val Ile Gln Ile Thr
435 440 445

Arg Met Asn Lys Asp Lys Thr Arg Lys Ala Arg Ala Val Ile Asn Leu
450 455 460

Lys Asn Leu Thr Tyr Gln Val Thr Val Asn Asn Glu Val Ile Asn Phe
465 470 475 480

<210> 19
<211> 1443
<212> DNA
<213> *Listeria monocytogenes*

<220>
<221> CDS
<222> (1)..(1443)

<400> 19
atg caa att aaa aat aaa gct atg tta att act tat tct gat agt tta 48
Met Gln Ile Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Leu
1 5 10 15

ggg aaa aat atg gaa gaa tta tcc aag gtg atg gaa act tat ttt gaa 96
Gly Lys Asn Met Glu Glu Leu Ser Lys Val Met Glu Thr Tyr Phe Glu
20 25 30

gat gct gtt ggc ggg att cac tta ttg ccg ttc ttt cca tcc act gga 144
Asp Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

gat cga ggg ttt gcg cca agt gat tac aca aca gta gat agc gac cta 192
Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Thr Val Asp Ser Asp Leu
50 55 60

ggg tct tgg gaa ata atc gag aaa tta ggc gaa aag tat tat tta atg 240
Gly Ser Trp Glu Ile Ile Glu Lys Leu Gly Glu Lys Tyr Tyr Leu Met
65 70 75 80

ttt gat ttt atg att aat cac att tct cgc gaa tca ctc ttc ttt caa 288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Leu Phe Phe Gln
85 90 95

gat ttt aaa aaa gag cat tta aac tca aag tat aaa gat atg ttt att 336
Asp Phe Lys Lys Glu His Leu Asn Ser Lys Tyr Lys Asp Met Phe Ile
100 105 110

cgt atc aat gat ttc ttt cct ccg ggt aga cca aat gaa aaa gac tta 384
Arg Ile Asn Asp Phe Phe Pro Pro Gly Arg Pro Asn Glu Lys Asp Leu
115 120 125

gat tta att tat aag aga aaa gat aag gcg cct ttt caa gaa gtt gaa 432
Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Phe Gln Glu Val Glu
130 135 140

ttt gct gat ggg gga acg gaa tta gtt tgg aat act ttt ggg gaa gaa 480
Phe Ala Asp Gly Gly Thr Glu Leu Val Trp Asn Thr Phe Gly Glu Glu
145 150 155 160

caa att gat tta gat gtg aca gcc gaa gtt aca aaa gaa ttt att cgt 528
Gln Ile Asp Leu Asp Val Thr Ala Glu Val Thr Lys Glu Phe Ile Arg
165 170 175

caa acg ata aaa aat atg gct gca cat ggt tgt tct att ttg cgt ctt 576
Gln Thr Ile Lys Asn Met Ala Ala His Gly Cys Ser Ile Leu Arg Leu
180 185 190

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gat gcc ttt gct tat gca att aaa aaa tta gat aca aat gat ttt ttt 624
Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205

gta gaa ccg gaa att tgg gat tta ctg gat gaa gtg aaa gca gaa gcg 672
Val Glu Pro Glu Ile Trp Asp Leu Leu Asp Glu Val Lys Ala Glu Ala
210 215 220

gcc aaa tat gac atg gaa tta tta cca gaa att cat gaa cat tat tcc 720
Ala Lys Tyr Asp Met Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
225 230 235

atc caa atg aaa atc gcg aac cat gat tat tat atc tat gat ttt gcg 768
Ile Gln Met Lys Ile Ala Asn His Asp Tyr Tyr Ile Tyr Asp Phe Ala
245 250 255

tta ccc atg gtg atg ctg tac tgc tta tat agt ggc cga gtg gaa cgt 816
Leu Pro Met Val Met Leu Tyr Ser Leu Tyr Ser Gly Arg Val Glu Arg
260 265 270

tta gct aaa tgg tta gaa atg agt ccg atg aag caa ttt act act tta 864
Leu Ala Lys Trp Leu Glu Met Ser Pro Met Lys Gln Phe Thr Thr Leu
275 280 285

gat acg cat gat ggc att ggc gtt gtg gat gca cgc gat tta tta aca 912
Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Leu Leu Thr
290 295 300

gat gag gaa ctc gat tat act tca gca gaa tta tac aaa ata gga gct 960
Asp Glu Glu Leu Asp Tyr Thr Ser Ala Glu Leu Tyr Lys Ile Gly Ala
305 310 315

aat gtt aaa aag ata tat tcc tct gaa aaa tat aat aac ctg gat att 1008
Asn Val Lys Lys Ile Tyr Ser Ser Glu Lys Tyr Asn Asn Leu Asp Ile
325 330 335

tat caa att aat agt acc tat tat agt gct ttg ggt gac gat gat aaa 1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
340 345 350

agt tac ttg tta gcg aga gta att caa tgt ttt gcg ccg ggg att ccg 1104
Ser Tyr Leu Leu Ala Arg Val Ile Gln Cys Phe Ala Pro Gly Ile Pro
355 360 365

caa att tat tat gtt ggt tta ctt gct ggc aaa aat gat att gac ctt 1152
Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Ile Asp Leu
370 375 380

tta gag gaa aca aaa gaa ggg cgt aat att aat cgt cat tac tac aca 1200
Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Thr
385 390 395

ata gat gaa att aaa aat gaa gta aaa aga cca gtt gtt aaa gcg ttg 1248
Ile Asp Glu Ile Lys Asn Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415

tgc aat tta ctg agg ttt aga aat act tct gaa gcg ttt gat ttg gaa 1296
Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu
420 425 430

gga agt ata gaa att gag aca cct agc tca aat gaa atc gtt att att 1344
Gly Ser Ile Glu Ile Glu Thr Pro Ser Ser Asn Glu Ile Val Ile Ile
435 440 445

cgc aaa aac aaa aca aat aaa att aca gcg aca tta aaa gca aat tta 1392
Arg Lys Asn Lys Thr Asn Lys Ile Thr Ala Thr Leu Lys Ala Asn Leu
450 455 460

agt act aaa aca ttc caa atc agc gaa aat gaa aga aat att tta att 1440
Ser Thr Lys Thr Phe Gln Ile Ser Glu Asn Glu Arg Asn Ile Leu Ile
465 470 475

taa 1443

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<210> 20
<211> 480
<212> PRT
<213> Listeria monocytogenes

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<400> 20
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Met Gln Ile Lys Asn Lys Ala Met Leu Ile Thr Tyr Ser Asp Ser Leu
1 5 10 15

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Gly Lys Asn Met Glu Glu Leu Ser Lys Val Met Glu Thr Tyr Phe Glu
 20 25 30
 Asp Ala Val Gly Gly Ile His Leu Leu Pro Phe Phe Pro Ser Thr Gly
 35 40 45
 Asp Arg Gly Phe Ala Pro Ser Asp Tyr Thr Thr Val Asp Ser Asp Leu
 50 55 60
 Gly Ser Trp Glu Ile Ile Glu Lys Leu Gly Glu Lys Tyr Tyr Leu Met
 65 70 75 80
 Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Leu Phe Phe Gln
 85 90 95
 Asp Phe Lys Lys Glu His Leu Asn Ser Lys Tyr Lys Asp Met Phe Ile
 100 105 110
 Arg Ile Asn Asp Phe Phe Pro Pro Gly Arg Pro Asn Glu Lys Asp Leu
 115 120 125
 Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Phe Gln Glu Val Glu
 130 135 140
 Phe Ala Asp Gly Gly Thr Glu Leu Val Trp Asn Thr Phe Gly Glu Glu
 145 150 155 160
 Gln Ile Asp Leu Asp Val Thr Ala Glu Val Thr Lys Glu Phe Ile Arg
 165 170 175
 Gln Thr Ile Lys Asn Met Ala Ala His Gly Cys Ser Ile Leu Arg Leu
 180 185 190
 Asp Ala Phe Ala Tyr Ala Ile Lys Lys Leu Asp Thr Asn Asp Phe Phe
 195 200 205
 Val Glu Pro Glu Ile Trp Asp Leu Leu Asp Glu Val Lys Ala Glu Ala
 210 215 220
 Ala Lys Tyr Asp Met Glu Leu Leu Pro Glu Ile His Glu His Tyr Ser
 225 230 235 240
 Ile Gln Met Lys Ile Ala Asn His Asp Tyr Tyr Ile Tyr Asp Phe Ala
 245 250 255
 Leu Pro Met Val Met Leu Tyr Ser Leu Tyr Ser Gly Arg Val Glu Arg
 260 265 270
 Leu Ala Lys Trp Leu Glu Met Ser Pro Met Lys Gln Phe Thr Thr Leu
 275 280 285
 Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp Leu Leu Thr
 290 295 300
 Asp Glu Glu Leu Asp Tyr Thr Ser Ala Glu Leu Tyr Lys Ile Gly Ala
 305 310 315 320
 Asn Val Lys Lys Ile Tyr Ser Ser Glu Lys Tyr Asn Asn Leu Asp Ile
 325 330 335
 Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys
 340 345 350

Ser Tyr Leu Leu Ala Arg Val Ile Gln Cys Phe Ala Pro Gly Ile Pro
355 360 365

Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Ile Asp Leu
370 375 380

Leu Glu Glu Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Thr
385 390 395 400

Ile Asp Glu Ile Lys Asn Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415

Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu
420 425 430

Gly Ser Ile Glu Ile Glu Thr Pro Ser Ser Asn Glu Ile Val Ile Ile
435 440 445

Arg Lys Asn Lys Thr Asn Lys Ile Thr Ala Thr Leu Lys Ala Asn Leu
450 455 460

Ser Thr Lys Thr Phe Gln Ile Ser Glu Asn Glu Arg Asn Ile Leu Ile
465 470 475 480

<210> 21
<211> 1443
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutant of Streptococcus mutans sucrose phyophorylase

<220>
<221> CDS
<222> (1)..(1443)

<400> 21
atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg 48
Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1 5 10 15
ggg aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga 96
Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
20 25 30
gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc tca ggt 144
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly
35 40 45
gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac cct gct ttt 192
Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Pro Ala Phe
50 55 60
ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa cat tac ctc atg 240
Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met
65 70 75 80
ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa 288
Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
85 90 95
gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta 336
Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
100 105 110
aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat ctg 384
Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Leu
115 120 125
gac ctg att tat aag cgt aag gat cga gca cct atg cag gaa atc cga 432
Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Met Gln Glu Ile Arg
130 135 140
ttt gca gat ggc agt gtt gaa cat ctc tgg agc act ttt ggg gag gaa 480
Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu

145	150	155	160	
cag att gat ctt gac glg act aaa gaa glg act atg gat ttt att cgc				528
Gln Ile Asp Leu Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg	165	170	175	
tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg				576
Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu	180	185	190	
gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt				624
Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe	195	200	205	
ggt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct				672
Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala	210	215	220	
gct gta tgc ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act				720
Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr	225	230	235	240
att caa ttt aaa att gca gac cat ggt tac tat gtt tat gat ttt gcc				768
Ile Gln Phe Lys Ile Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala	245	250	255	
ctg cct atg gtg acg ctc tac agc cta tat tgc ggc aag gtt gac cgt				816
Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg	260	265	270	
ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt				864
Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu	275	280	285	
gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act				912
Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr	290	295	300	
gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc				960
Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala	305	310	315	320
aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc				1008
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile	325	330	335	
tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa				1056
Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln	340	345	350	
aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca				1104
Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro	355	360	365	
cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta				1152
Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu	370	375	380	
ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt				1200
Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser	385	390	395	400
agt gaa gaa att gct aag gaa gtg aag ccg cca gtt gtc aag gca ctt				1248
Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu	405	410	415	
tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat				1296
Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp	420	425	430	
ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa				1344
Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu	435	440	445	
cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc				1392
Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu	450	455	460	
caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt				1440
Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe	465	470	475	480
gaa				1443
Glu				

<210> 22
 <211> 481
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22

Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
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Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
 20 25 30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly
 35 40 45

Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Pro Ala Phe
 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met
 65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
 85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
 100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Leu
 115 120 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Met Gln Glu Ile Arg
 130 135 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu
 145 150 155 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
 165 170 175

Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
 195 200 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
 210 215 220

Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
 225 230 235 240

Ile Gln Phe Lys Ile Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala
 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr

290 295 300

Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305 310 315 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
325 330 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
340 345 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
355 360 365

Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 375 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
420 425 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
435 440 445

Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
450 455 460

Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe
465 470 475 480

Glu

<210> 23
<211> 1461
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutant of Streptococcus mutans sucrose phosphorylase

<220>
<221> CDS
<222> (1)..(1461)

<400> 23
atg cca att aca aat aaa aca atg ttg att act tac gca gac agt ttg 48
Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1 5 10 15
ggg aaa aat ttg aaa gaa ttg aat gaa aat att gag aat tat ttt gga 96
Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
20 25 30
gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt 144
Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45
gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt 192
Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
50 55 60
ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg 240
Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65 70 75 80

ttt gat ttc atg att aat cat att tcg cgt cag tct aaa tat tat aaa Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95	288
gat tac caa gaa aag cat gaa gca agt gct tat aaa gat cta ttt tta Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu 100 105 110	336
aat tgg gat aaa ttt tgg cct aaa aat cgc ccg aca caa gaa gat gtg Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val 115 120 125	384
gac ctg att tat aag cgt aag gat cga gca cct aag cag gaa atc caa Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln 130 135 140	432
ttt gca gat ggc agt gtt gaa cat ctc tgg aac act ttt ggg gag gaa Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160	480
cag att gat ctt gac gtg act aaa gaa gtg act atg gat ttt att cgc Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg 165 170 175	528
tct acc att gaa aat tta gca gcc aac ggc tgt gat ctc att cgt ttg Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu 180 185 190	576
gat gcc ttt gct tat gct gtt aaa aag cta gat acg aat gat ttc ttt Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205	624
gtt gaa cct gaa atc tgg act ctg cta gat aaa gtt cgt gat ata gct Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala 210 215 220	672
gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat act Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr 225 230 235 240	720
att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcc Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255	768
ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cgt Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 265 270	816
ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ctt Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu 275 280 285	864
gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg act Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr 290 295 300	912
gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gcc Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 315 320	960
aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat atc Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335	1008
tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat caa Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln 340 345 350	1056
aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cca Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro 355 360 365	1104
cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tta Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu 370 375 380	1152
ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat agt Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser 385 390 395 400	1200
agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ctt Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415	1248
tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg gat	1296

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
420 425 430

ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata gaa 1344
Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
435 440 445

cgt caa aat aaa gat ggc agt cat atc gca aca gca gag att aat ctc 1392
Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
450 455 460

caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc tta 1440
Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Leu
465 470 475 480

tcc atg ata agc tgt caa aca 1461
Ser Met Ile Ser Cys Gln Thr
485

<210> 24
<211> 487
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

Met Pro Ile Thr Asn Lys Thr Met Leu Ile Thr Tyr Ala Asp Ser Leu
1 5 10 15

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly
20 25 30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35 40 45

Asp Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe
50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met
65 70 75 80

Phe Asp Phe Met Ile Asn His Ile Ser Arg Gln Ser Lys Tyr Tyr Lys
85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu
100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gln Glu Asp Val
115 120 125

Asp Leu Ile Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gln Glu Ile Gln
130 135 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu
145 150 155 160

Gln Ile Asp Leu Asp Val Thr Lys Glu Val Thr Met Asp Phe Ile Arg
165 170 175

Ser Thr Ile Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu Ile Arg Leu
180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe
195 200 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala
210 215 220

Ala Val Ser Gly Ala Glu Ile Leu Pro Glu Ile His Glu His Tyr Thr
225 230 235 240

Ile Gln Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala
245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg
260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu
275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr
290 295 300

Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305 310 315 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile
325 330 335

Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gln
340 345 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro
355 360 365

Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 375 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser
385 390 395 400

Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp
420 425 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu
435 440 445

Arg Gln Asn Lys Asp Gly Ser His Ile Ala Thr Ala Glu Ile Asn Leu
450 455 460

Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Leu
465 470 475 480

Ser Met Ile Ser Cys Gln Thr
485

<210> 25
<211> 56
<212> PRT
<213> Streptococcus mutans

<400> 25

Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly Asp
1 5 10 15

Arg Gly Phe Ala Pro Ile Asp Tyr His Glu Val Asp Ser Ala Phe Gly
20 25 30

Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met Phe

35

40

45

Asp Phe Met Ile Asn His Ile Ser
50 55

<210> 26

<211> 42

<212> PRT

<213> Streptococcus mutans

<400> 26

Arg Pro Thr Gln Glu Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Arg
1 5 10 15

Ala Pro Lys Gln Glu Ile Gln Phe Ala Asp Gly Ser Val Glu His Leu
20 25 30

Trp Asn Thr Phe Gly Glu Glu Gln Ile Asp
35 40

<210> 27

<211> 38

<212> PRT

<213> Streptococcus mutans

<400> 27

Ile Leu Pro Glu Ile His Glu His Tyr Thr Ile Gln Phe Lys Ile Ala
1 5 10 15

Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala Leu Pro Met Val Thr Leu
20 25 30

Tyr Ser Leu Tyr Ser Gly
35